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Expanded description of *Hemiphyllodactylus hongkongensis* (Squamata, Gekkonidae)

Xiang-Yi Li[1], Shi-Shi Lin[2], Zhao-Chi Zeng[3], Yan-Jun Sun[4], Jian Wang[3]

1 *Guangdong Zhongtai Environmental Protection Technology Co., LTD, Maoming 525099, China*
2 *Guangdong Polytechnic of Environmental Protection Engineering, Foshan 528216, China*
3 *Shenzhen Academy of Environmental Sciences, Shenzhen 518022, China*
4 *Guangdong Eco-Engineering Polytechnic, Guangzhou 510520, China*

https://zoobank.org/C4FC529A-B70C-4E9E-9239-586ADA4D140A

Corresponding authors: Jian Wang (wangj-1994@outlook.com); Yan-Jun Sun (gstsyj2023@163.com)

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Abstract

The expanded description of *Hemiphyllodactylus hongkongensis* Sung, Lee, NG, Zhang & Yang, 2018 is provided based on four newly collected specimens from eastern Guangdong Province, China, which is beyond its previously known range. The new collection also fills the distribution gap of the genus *Hemiphyllodactylus* in the region. Due to the absence of sufficient data, we recommend *Hemiphyllodactylus hongkongensis* be listed as Data Deficient (DD) in the IUCN conservation status categorization.

Key Words

conservation, molecular phylogeny, morphology, slender gecko

Introduction

The genus *Hemiphyllodactylus* Bleeker, 1860, commonly known as the half leaf-fingered geckos, dwarf geckos or slender geckos, are a group of extremely diverse yet morphologically conserved lizards that are widespread in the Indo-Pacific realm with 54 recognized species (Zug 2010; Grismer et al. 2013; Agarwal et al. 2019; Agung et al. 2021, 2022; Uetz et al. 2023). The rapid advancement and application of molecular techniques in taxonomic studies have led to a great increase in the discovery of cryptic species in recent years (Zug et al. 2010; Grismer et al. 2013; Grismer et al. 2015; Cobos et al. 2016; Grismer et al. 2018; Agarwal et al. 2019; Grismer et al. 2020).

The Hong Kong Slender Gecko, *Hemiphyllodactylus hongkongensis* Sung, Lee, NG, Zhang & Yang, 2018 was originally described based on two male and six female specimens from Aberdeen Country Park (22°15.51'N, 114°9.69'E; 120 m a.s.l.) and Po Toi Island (22°9.83'N, 114°15.33'E; 50 m a.s.l.), Hong Kong SAR, China, with molecular evidence in the mitochondrial ND2 gene and the following diagnostic characters: (1) 5–6 chin scales in a unique combination, (2) manual lamellar formula 3-3(4)-4-4, (3) pedal lamellar formula 3(4)-4(5)-4(5)-4, (4) 24–25 continuous femoral and precloacal pores, (5) 12–15 dorsal scales contained in diameter of eye, (6) 9–10 ventral scales contained in diameter of eye (Sung et al. 2018). It was previously thought to be endemic to Hong Kong. However, during recent herpetological surveys in eastern Guangdong Province, China where there is no record of the genus *Hemiphyllodactylus*, we collected four specimens which generally match the morphological diagnosis of *H. hongkongensis* but also show variations in the manual lamellar formula, pedal lamellar formula, the number of continuous femoral and precloacal pores, dorsal and ventral scales contained in diameter of eye. Subsequent phylogenetic analysis demonstrates the newly collected specimens to be conspecific with *H. hongkongensis*

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with subtle genetic divergences. Herein, a detailed morphological redescription includes the revised diagnostic characters, sexual dimorphism and ecology information, as well as the expanded geography range are provided.

Materials and methods

Morphometrics

Morphological examinations were performed on the four newly collected specimens from eastern Guangdong Province, China (Fig. 1). The collection information is given in the taxonomy account below. All specimens were fixed in 10% buffered formalin and later transferred to 70% ethanol for preservation, and deposited at the Guangdong Polytechnic of Environmental Protection Engineering (GEP), Foshan City, Guangdong, China; tissue samples were preserved in 95% ethanol for molecular studies.

Measurements followed Zug. (2010) and were taken with a digital caliper to the nearest 0.1 mm. These measurements are as follows: snout-vent length (SVL, distance from the tip of snout to the vent), tail length (TailL, from the vent to the tip of tail), trunk length (TrunkL, taken from the posterior margin of the forelimb at its insertion point on the body to the anterior margin of the hind limb at its insertion point on the body), eye diameter (EyeD, the horizontal diameter of the eyeball); head length (HeadL, distance between retroarticular process of jaw to snout-tip), head width (HeadW, maximum width of head), nares-eye length (NarEye, measured from the anterior margin of the eye ball to the posterior margin of the external nares), snout-eye length (SnEye, distance between anterior most point of eye and the tip of snout), internarial width (SnW, distance between external nares). Evaluation of meristic characters and color pattern followed Zug (2010) and Grismer et al. (2013).

Phylogenetic analyses

In total, 156 samples including four outgroup samples were used in this study, encompassing four newly sequenced individuals and others downloaded from GenBank. Detailed information for all samples was given in Suppl. material 1.

The NADH dehydrogenase subunit 2 gene (*ND2*) fragment was amplified for new samples with the primers ND2f101A and HemiR followed Sung et al. (2018). DNA extraction, PCR, and sequencing followed Agung et al. (2022). Sequences were aligned with Clustal X 2.0 (Thompson et al. 1997) with default parameters. PartitionFinder2 was used to test the best partitioning scheme and jModelTest v2.1.2 was used to test the best fitting nucleotide substitution models, resulting the *ND2* gene partitioned by codon position, and the best fit models

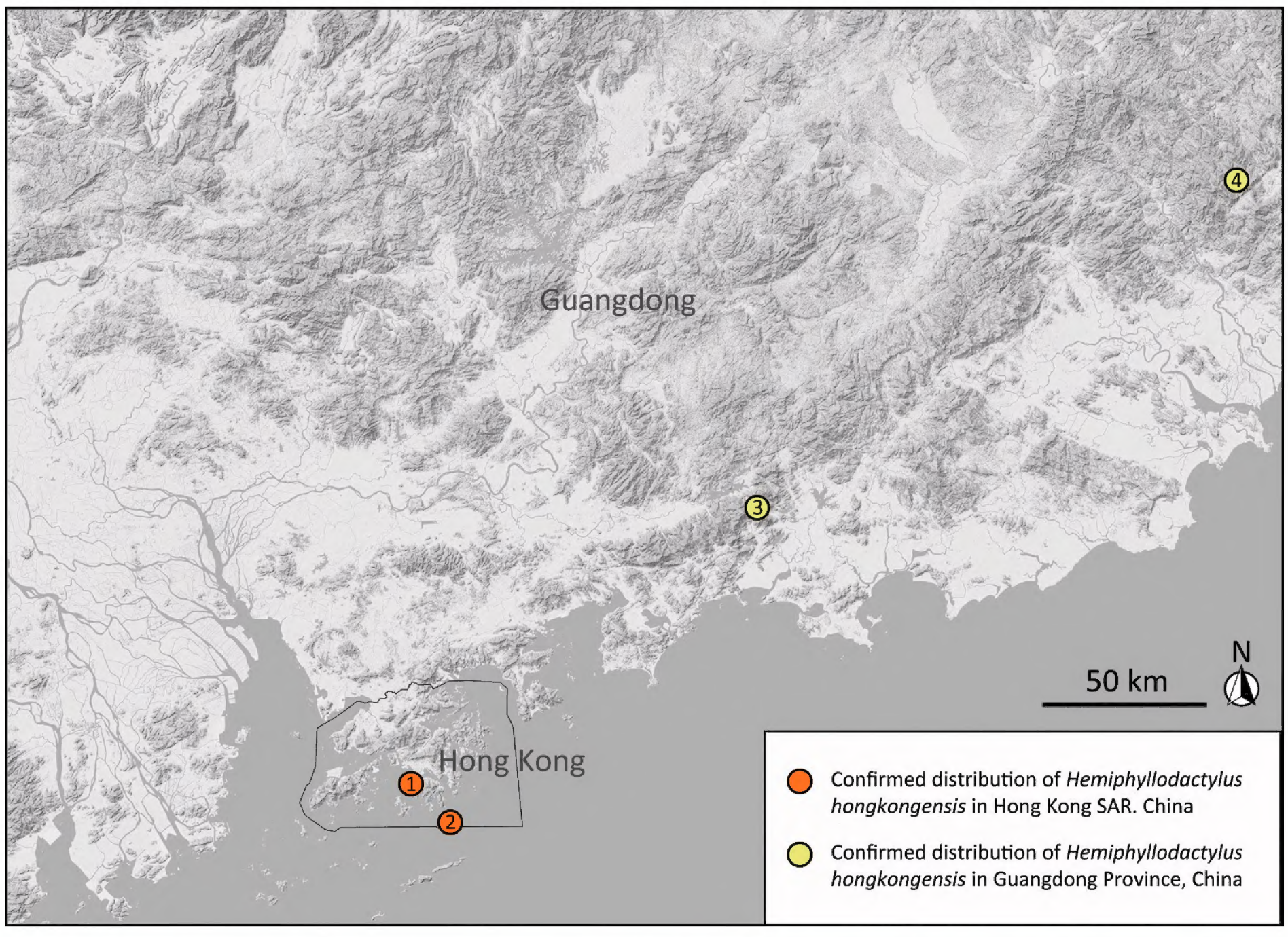

Figure 1. Map showing the confirmed distribution of *Hemiphyllodactylus hongkongensis*: Aberdeen Country Park **(1)** and Po Toi Island **(2)**, Hong Kong SAR, China, and Mt. Lianhua **(3)** and Mt. Fenghuang **(4)**, Guangdong Province, China.

for all partitions was GTR+I+G (General Time Reversible model, with variable sites modelled according to the Gamma distribution, and a portion of the sites invariant). Phylogenetic analysis was conducted using Bayesian inference (BI) in MrBayes 3.2.4 (Ronquist et al. 2012) and maximum likelihood (ML) in maximum likelihood (ML) in Randomized Axelerated Maximum Likelihood (RAxML, Stamatakis 2006) with RAxML GUI 1.3 (Silvestro and Michalak 2012). For the ML analysis, an optimal tree was obtained and branch supports were evaluated with 1000 rapid bootstrapping replicates. For the BI analysis, two independent runs with four Markov Chain Monte Carlo simulations were performed for ten million iterations and sampled every 1000 iterations. The first 25% of the samples were discarded as burn-in, leaving 7500 samples in the final summary. Convergence of the Markov Chain Monte Carlo simulations was assessed by PSRF < 0.01 and ESS (effective sample size) value > 200 using Tracer 1.4 (http://tree.bio.ed.ac.uk/software/tracer/). Nodes having ML bootstrap values (BS) ≥ 70 and BI posterior probabilities (BPP) ≥ 0.90 were considered well supported. Genetic distances among *Hemiphyllodactylus hongkongensis* with its phylogenetically close congeners were calculated in MEGA 6 using the uncorrected *p*-distance model.

Results

The ML and Bayesian results show identical topologies, and all *Hemiphyllodactylus* samples form a monophyletic clade with strongly-support in both phylogenetic trees (Fig. 2). *Hemiphyllodactylus hongkongensis*, *H. yanshanensis*, *H. huishuiensis*, *H. nahanensis*, *H. dushanensis*, *H. dupanglingensis*, *H. zugi* and *H. ngocsonensis* form a robust clade (BS = 100; BPP = 1.00), and their uncorrected *p*-distance are calculated and listed in Suppl. material 2. In addition, the *Hemiphyllodactylus* samples from Mt. Lianhua and from Mt. Fenghuang cluster with topotypic samples of *H. hongkongensis* with shallow divergence (BS = 100; BPP = 1.00; *p*-distance 0.002–0.017). This result indicates that the newly collected specimens from eastern Guangdong should be identified as *H. hongkongensis*.

Taxonomic account

Hemiphyllodactylus hongkongensis Sung, Lee, NG, Zhang & Yang, 2018

Fig. 3

Hong Kong Slender Gecko / xiāng gǎng bàn yè zhǐ hǔ (香港半叶趾虎)

Chresonymy. *Hemiphyllodactylus* sp. – Chan et al. 2018.

Examined materials. GEP r024, adult male, and GEP r025–026, adult females, collected by Jian Wang and Zhao-Chi Zeng from Mt. Fenghuang (26°54'33.61"N, 116°36'26.51"E; ca. 1180 m a.s.l.), Chaozhou City, Guangdong Province, China. GEP r032, adult male, collected by Jian Wang and Zhao-Chi Zeng from Mt. Lianhua (23°4'3.51"N, 115°14'14.39"E; ca. 870 m a.s.l.), Huizhou City, Guangdong Province, China.

Description of new specimens. Morphometric data are listed in Tables 1, 2. Head triangular in dorsal profile, depressed, distinct from neck; lores and interorbital regions flat; rostrum relatively long (NarEye/HeadL 0.27–0.33); prefrontal region flat; canthus rostralis smoothly rounded, snout moderate, rounded in dorsal profile; eye large (EyeD/HeadL 0.22–0.24, EyeD/NarEye 0.80–0.84); ear opening oval, small; eye to ear distance greater than diameter of eye; rostral wider than high, bordered posteriorly by large supranasals; 1–3 internasals in contact with rostral anteriorly; circumnasals 3–4; supralabials 10–13; infralabials 9–12; dorsal superciliaries flat, rectangular, imbricate; mental triangular, bordered laterally by first infralabials and posteriorly by two (GEP r024–026) or three (GEP r032) large postmentals; gular scales triangular small, granular, grading posteriorly into slightly larger, subimbricate, throat and pectoral scales which grade into slightly larger, subimbricate ventrals.

Body slender and small, dorsoventrally compressed, ventrolateral folds absent; dorsal scales small, granular, 18–20 scales contained within one eye diameter; ventral scales, flat, subimbricate, larger than dorsal scales, 10–13 scales contained within one eye diameter; in males, 23–24 pore-bearing scales extending from midway between the knee and hind limb insertion of one leg to the other.

Forelimbs short, robust in stature, covered with granular scales dorsally and with slightly larger, flat, subimbricate scales ventrally; palmar scales flat, imbricate; all digits except digit I well developed; digit I vestigial, clawless; distal, subdigital lamellae of digits II–V undivided, angular and fan-shaped; lamellae proximal to these transversely expanded; lamellar formula of digits II–V 3–4–4(5)–4 on both hands; 4–5 transversely expanded lamellae on digit I; claws on digits II–V well-developed, unsheathed; distal portions of digits strongly curved, terminal joint free, arising from central portion of lamellar pad. Hind limbs short, more robust than forelimbs, covered with slightly pointed, juxtaposed scales dorsally and by larger, flat subimbricate scales ventrally; all digits except digit I well-developed; digit I vestigial, clawless; distal, subdigital lamellae of digits II–V undivided, angular and fan-shaped; lamellae proximal to these transversely expanded; lamellar formula of digits II–V 4–4(5)–4(5)–4(5); 4–5 transversely expanded lamellae on digit I; claws on digits II–V well-developed, unsheathed; distal portions of digits strongly curved, terminal joint free, arising from central portion of lamellar pad; posterior section of tail broken, round in cross-section; all caudal scales flat, subimbricate, not forming distinct caudal segments.

Coloration of new specimens in life. Dorsal surface of head, body, and limbs pale-brown, densely mottled with irregular darker markings; a dark brown preorbital tripe extending from external nares to anterior corner of eye; a dark brown postorbital tripe through extending from posterior corner of eye to just anterior of forelimb insertion

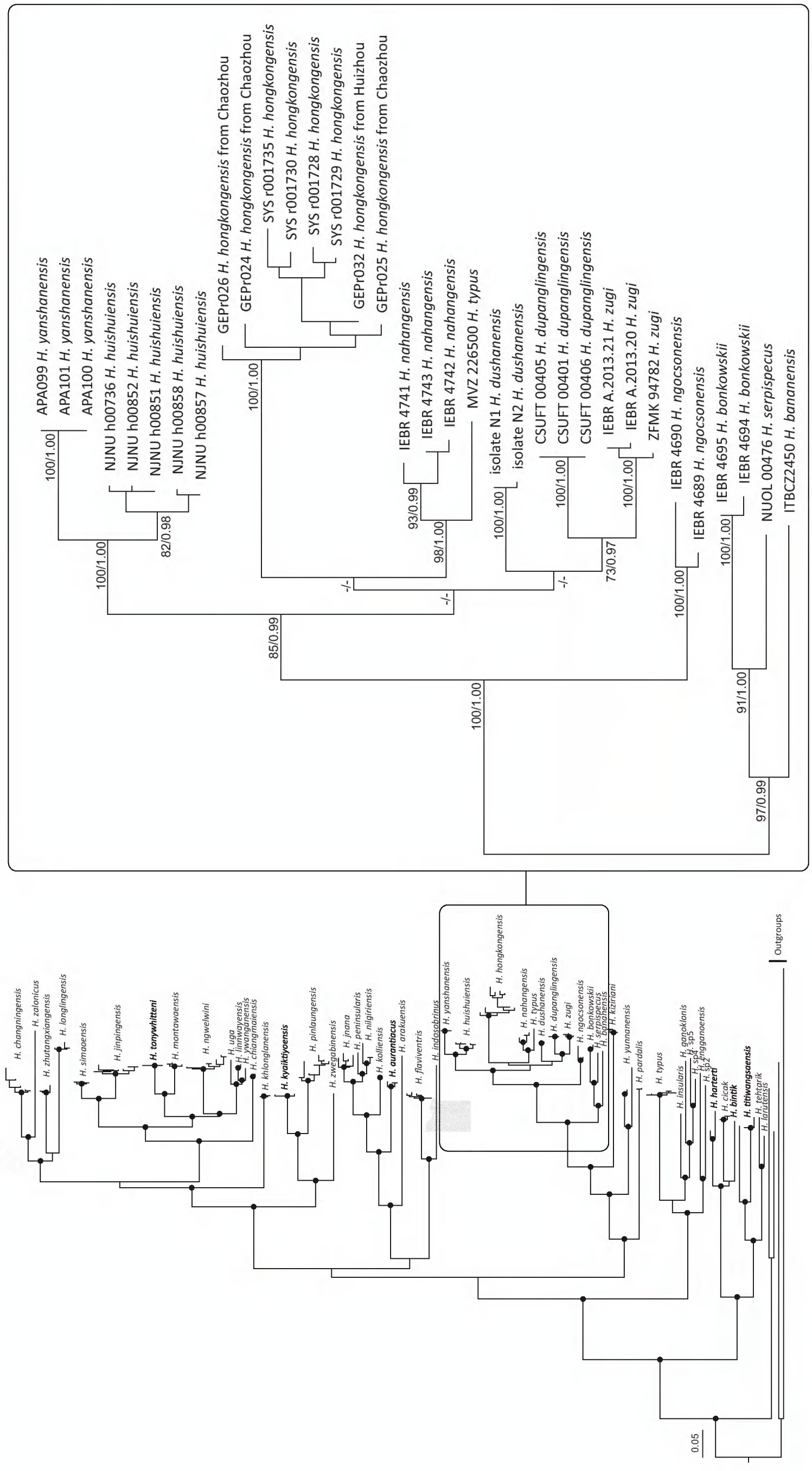

Figure 2. Bayesian Inference and Maximum Likelihood phylogenies. Black dots at nodes in the left part of the trees represents the Bayesian posterior probabilities (BPP) > 0.90 and the bootstrap supports (BS) > 70. Numbers at nodes in the right part of the tree represents the BS/BPP and '-' represents Bayesian posterior probabilities (BPP) < 0.90 or the bootstrap supports (BS) < 70.

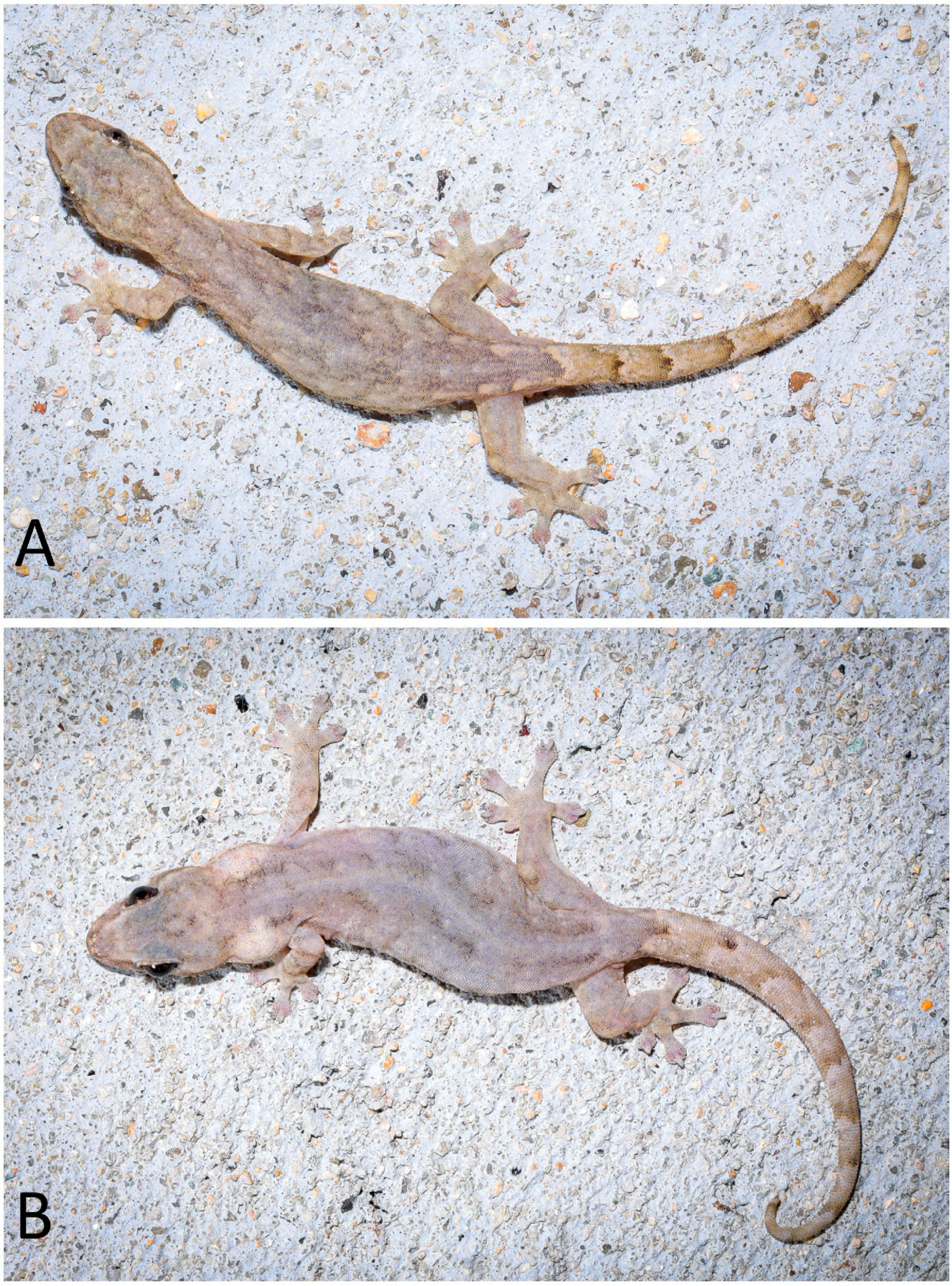

Figure 3. Life aspect of *Hemiphyllodactylus hongkongensis* **A.** Male (GEP r032) and **B.** Female (uncaptured) from Mt. Lianhua, Huizhou City, Guangdong Province, China. Photos by Jian Wang.

on body; limbs and digits with irregularly shaped dark markings; ventral head, body and limbs unicolor beige; dorsal tail olive-brown, with several irregularly shaped dark markings and gray-white mottling, ventral tail unicolor gray-brown.

Coloration of new specimens in preservative. Dorsal surface of head, body, limbs and tail dorsal dark brown, irregular darker markings more distinct; ventral head, body and limbs gray-brown; pre- and postorbital tripes, irregularly shaped dark markings on limbs and digits, dark

Table 1. Scalation of *Hemiphyllodactylus hongkongensis*.

Vocher	SYS r001735 (Holotype)	SYS r001734 (Paratype)	GEP r024	GEP r032	SYS r001728 (Paratype)	SYS r001729 (Paratype)
Sex	Male	Male	Male	Male	Female	Female
Dorsal scales	15	14	19	20	13	14
Ventral scales	10	9	13	12	10	9
Cloacal spurs on each side	1	1	1	1	1	1
Circumnasal scales	3	3	4	3/4	3	3
Scales between supranasals	3	3	2	3	3	3
Supralabial scales	10/10	11/11	11/13	12/10	11/11	12/12
Infralabial scales	9/10	10/11	10/11	10/11	10/10	10/10
Chin scales	5	6	6	6	6	5
Manual lamellar formula	3444	3444	3454	3444	3444	3444
Pedal lamellar formula	4554	4554	4554	4445/4554	4444	4554
Subdigital lamellae on 1st finger	5	5	4	5	4	4
Subdigital lamellae on 1st toe	5	5	4	5	5	5
Precloacal and femoral pores	24	25	24	23	0	0
Vocher	**SYS r001730 (Paratype)**	**SYS r001731 (Paratype)**	**SYS r001732 (Paratype)**	**SYS r001733 (Paratype)**	**GEP r025**	**GEP r026**
Sex	Female	Female	Female	Female	Female	Female
Dorsal scales	13	12	14	13	18	20
Ventral scales	9	9	9	10	10	12
Cloacal spurs on each side	1	1	0	1	1	1
Circumnasal scales	3	3	4	3	3	3
Scales between supranasals	3	4	3	3	2	1
Supralabial scales	12/12	10/10	12/11	11/11	13/12	11/11
Infralabial scales	10/10	10/10	11/10	11/10	11/9	10/12
Chin scales	6	6	5	6	6	6
Manual lamellar formula	3444	3344	3444	3444	3444	3444
Pedal lamellar formula	4554	3444	4554	4554	4554	4554
Subdigital lamellae on 1st finger	4	3	4	4	4	4
Subdigital lamellae on 1st toe	5	5	5	5	5	4
Precloacal and femoral pores	0	0	0	0	0	0

markings on dorsal tail more distinct; gray-white mottling on dorsal tail absent; ventral tail unicolor dark brown.

Sexual dimorphism. Males possess a pair of hemipenis and 23–25 precloacal and femoral pores; gravid females harbor two calcareous eggs.

Revision of diagnostic characters. (1) 5–6 chin scales in the unique combination, (2) manual lamellar formula 3-3(4)-4(5)-4, (3) pedal lamellar formula 3(4)-4(5)-4(5)-4(5), (4) 23–25 continuous femoral and precloacal pores, (5) 12–20 dorsal scales contained in diameter of eye, (6) 9–13 ventral scales contained in diameter of eye.

Distribution and ecology. *Hemiphyllodactylus hongkongensis* is currently known at low altitude from Aberdeen Country Park (ca. 120 m a.s.l.) and Po Toi Island (ca. 50 m a.s.l.), Hong Kong SAR, China, and Mt. Lianhua (ca. 870 m a.s.l.) and Mt. Fenghuang (ca. 1180 m a.s.l.) in eastern Guangdong Province, China. However, the taxonomic status of *Hemiphyllodactylus* populations from Shek Kwu Chau and Pokfulam Country Park in Hong Kong SAR, China still remained further confirmation (Karsen et al. 1998; Sung et al. 2018; Zug, 2010).

Hemiphyllodactylus hongkongensis is a forest dwelling species which can be found among the bark of large trees, abandoned buildings and rock crevices (Chan et al. 2008). Both newly discovered populations are found in the forest area at high altitude above ca. 800 m a.s.l.. Specimens from Mt. Lianhua are collected on the wall of an abandoned house, while those from Mt. Fenghuang are collected on the bare rocks. This species is oviparous so that each adult female including uncaptured individuals harbors two mature calcareous eggs during surveys on February (Mt. Lianhua) and July (Mt. Fenghuang).

Discussion

The genus *Hemiphyllodactylus* is an extremely diverse but taxonomically complicated group with dozens of morphological conservative congeners distributed in various habitats (Zug et al. 2010). The rapid advancement and application of molecular biology techniques have made great advancements in the taxonomic studies of this genus (Agarwal et al. 2019; Cobos et al. 2016; Grismer et al. 2013; Grismer et al. 2015; Grismer et al. 2018; Grismer et al. 2020; Zug et al. 2010). However, using single gene data, the phylogenetic relationships among *H. hongkongensis* and its genetically close congeners still remain unclear (Do et al. 2020; Sung et al. 2018; Zhang et al. 2020), More comprehensive genetic data from multiple populations are needed to solve this issue.

Even though the distribution range has been vastly expanded in this study, *Hemiphyllodactylus hongkongensis* likely has an even wider range in southeastern China due to its ability to adapt to diverse habitats in different elevations (see Distribution and ecology section above). More data based on exhaustive investiga-

Table 2. Measurements and body proportions of *Hemiphyllodactylus hongkongensis*.

Vocher	SYS r001735 (Holotype)	SYS r001734 (Paratype)	GEP r024	GEP r032	SYS r001728 (Paratype)	SYS r001729 (Paratype)
Sex	Male	Male	Male	Male	Female	Female
SVL	33.6	32.3	37.2	43.1	37.5	37.4
TailL	27.3	23.9	31.3	38.8	3.8	29.4
TrunkL	15.8	15.6	17.3	17.9	19.4	19.3
HeadL	9.3	8.7	9.7	10.4	9.5	9.9
HeadW	6.9	7.0	7.1	8.1	5.2	6.4
SnEye	3.1	3.2	3.8	3.9	3.2	3.7
NarEye	2.4	2.6	2.8	2.9	2.6	2.5
EyeD	2.0	2.3	2.3	2.4	2.2	2.3
SnW	1.1	1.1	1.1	1.2	1.2	1.1
TrunkL/SVL	0.47	0.48	0.47	0.42	0.52	0.52
HeadL/SVL	0.28	0.27	0.26	0.24	0.25	0.27
HeadW/SVL	0.21	0.22	0.19	0.19	0.14	0.17
HeadW/HeadL	0.74	0.80	0.73	0.78	0.55	0.64
SnEye/HeadL	0.33	0.37	0.39	0.38	0.33	0.37
NarEye/HeadL	0.26	0.30	0.28	0.33	0.27	0.26
EyeD/HeadL	0.22	0.27	0.24	0.22	0.24	0.23
SnW/HeadL	0.12	0.13	0.12	0.14	0.12	0.11
EyeD/NarEye	0.85	0.89	0.84	0.83	0.87	0.89
SnW/HeadW	0.24	0.23	0.17	0.19	0.33	0.28

Vocher	SYS r001730 (Paratype)	SYS r001731 (Paratype)	SYS r001732 (Paratype)	SYS r001733 (Paratype)	GEP r025	GEP r026
Sex	Female	Female	Female	Female	Female	Female
SVL	40.8	42.1	43.0	38.9	40.4	41.5
TailL	36.3	36.1	34.2	12.7	35.8	14.0 (broken tail)
TrunkL	21.0	21.3	22.0	20.4	20.4	18.8
HeadL	10.4	10.3	11.2	10.4	10.3	9.9
HeadW	8.0	7.5	8.2	8.2	7.2	8.0
SnEye	3.8	3.6	4.0	3.6	4.1	3.9
NarEye	2.9	3.1	3.0	3.0	2.8	2.7
EyeD	2.4	2.3	2.5	2.3	2.2	2.2
SnW	1.2	1.3	1.4	1.3	1.1	1.2
TrunkL/SVL	0.51	0.50	0.51	0.53	0.51	0.45
HeadL/SVL	0.26	0.24	0.26	0.27	0.26	0.24
HeadW/SVL	0.20	0.18	0.19	0.21	0.26	0.24
HeadW/HeadL	0.76	0.73	0.74	0.79	0.70	0.81
SnEye/HeadL	0.36	0.35	0.36	0.35	0.40	0.39
NarEye/HeadL	0.28	0.30	0.27	0.29	0.27	0.27
EyeD/HeadL	0.23	0.23	0.22	0.22	0.22	0.22
SnW/HeadL	0.11	0.12	0.12	0.12	0.16	0.17
EyeD/NarEye	0.81	0.76	0.82	0.78	0.80	0.81
SnW/HeadW	0.26	0.24	0.23	0.22	0.22	0.21

tions are still lacking in the mountain belt that stretches from Hongkong SAR and eastern Guangdong Province, to Fujian Province, China. Thus, we recommend *H. hongkongensis* be listed as Data Deficient (DD) in the IUCN categorization, pending further investigation. Moreover, the taxonomic status of *Hemiphyllodactylus* populations from Shek Kwu Chau and Pokfulam Country Park in Hong Kong SAR, China still require further confirmation (Karsen et al. 1998; Zug, 2010; Sung et al. 2018).

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Supplementary material 1

Localities, voucher information, and Genbank accession numbers for specimens used in this study

Authors: Xiang-Yi Li, Shi-Shi Lin, Zhao-Chi Zeng, Yan-Jun Sun, Jian Wang

Data type: xlsx

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Supplementary material 2

Pairwise distances based on ND2 gene among *Hemiphyllodactylus hongkongensis* and its phylogenetically close congeners

Authors: Xiang-Yi Li, Shi-Shi Lin, Zhao-Chi Zeng, Yan-Jun Sun, Jian Wang

Data type: xls

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